

RESULT 1
 AAY06483
 ID AAY06483 standard; Protein; 455 AA.
 XX
 AC AAY06483;
 XX
 DT 27-SEP-1999 (first entry)
 XX
 DE Human tumour-associated protein PRO347.
 XX
 KW PRO347; UNQ306; cancer; tumour; diagnosis; therapy; human.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..26
 FT /note= "signal peptide"
 FT Protein 27..455
 FT /note= "mature protein"
 FT Modified-site 144
 FT /note= "N-glycosylated"
 FT Domain 247..279
 FT /note= "EGF-like domain cysteine pattern signature"
 FT Domain 280..416
 FT /note= "EGF-like domain cysteine pattern signature"
 FT Domain 416..455
 FT /note= "C-type lectin domain signature"
 XX
 PN WO9935170-A2.
 XX
 PD 15-JUL-1999.
 XX
 PF 05-JAN-1999; 99WO-US00106.
 XX
 PR 20-NOV-1998; 98US-0109304.
 PR 05-JAN-1998; 98US-0070440.
 PR 29-APR-1998; 98US-0083500.
 PR 22-MAY-1998; 98US-0086414.
 PR 10-JUN-1998; 98US-0088742.
 PR 10-NOV-1998; 98US-0107783.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Botstein D, Goddard A, Gurney AL, Hillan KJ, Lawrence DA;
 PI Roy MA, Wood WI;
 XX
 DR WPI; 1999-430385/36.
 DR N-PSDB; AAX87260.
 XX
 PT Antibody against proteins expressed in neoplastic cells, useful for
 PT tumor diagnosis and treatment
 XX
 PS Example 1; Fig 14; 162pp; English.
 XX
 CC This sequence represents human PRO347 (UNQ306), a 50.5 kDa protein
 CC (pI 8.44) encoded by the novel cDNA clone DNA44176 (see AAX87260).
 CC Amplification of DNA44176 was observed in various tumour lines,
 CC suggesting a role in tumour formation and growth. Antagonists
 CC (e.g. antibodies) directed to PRO347 may have use in cancer therapy.
 CC The invention identifies 14 genes (see AAX87254-67) that are amplified
 CC in the genome of tumour cells. Such amplification is expected to be
 CC associated with overexpression of the gene product and to contribute
 CC to tumorigenesis. The encoded proteins (see AAY06477-90) may be
 CC useful targets for the diagnosis and/or treatment (including
 CC prevention) of certain cancers, and may act as predictors of the
 CC prognosis of tumour treatment. Antibodies that bind the proteins
 CC are claimed and used in claimed cancer diagnostic kits.
 XX
 SQ Sequence 455 AA;

 Query Match 100.0%; Score 2529; DB 20; Length 455;
 Best Local Similarity 100.0%; Pred. No. 1.7e-183;
 Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 MLHPETSPGRGHLLAVLLALLGTTWAEVWPPQLQEQAPMAGALNRKESFLLLSLHNR LRS 60
 Db 1 MLHPETSPGRGHLLAVLLALLGTTWAEVWPPQLQEQAPMAGALNRKESFLLLSLHNR LRS 60

 Qy 61 WVQPPAADMRRLDWSDSLAQLAQARAALCGIPTPSLASGLWRTLQVGWNNMQLLPAGLASF 120
 Db 61 WVQPPAADMRRLDWSDSLAQLAQARAALCGIPTPSLASGLWRTLQVGWNNMQLLPAGLASF 120

 Qy 121 VEVVSLWFAEGQRYSHAAGECARNATCTHYTQLVWATSSQLGCGRHLC SAGQTAIEAFVC 180
 Db 121 VEVVSLWFAEGQRYSHAAGECARNATCTHYTQLVWATSSQLGCGRHLC SAGQTAIEAFVC 180

 Qy 181 AYSPPGNWEVNGKTIIPYKKGAWCSLCTASVSGCFKAWDHAGGLCEVPRNPCRMSQNHG 240
 Db 181 AYSPPGNWEVNGKTIIPYKKGAWCSLCTASVSGCFKAWDHAGGLCEVPRNPCRMSQNHG 240

 Qy 241 RLNISTCHCHCPPGYTGRYCQVRCSLQCVHGRFREEECSVCVDIGYGGAQCATKVHFPFH 300
 Db 241 RLNISTCHCHCPPGYTGRYCQVRCSLQCVHGRFREEECSVCVDIGYGGAQCATKVHFPFH 300

 Qy 301 TCDLRIDGDCFMVSSEADTYRARMKCQRKGGVLAQIKSQKVQDILAFYLGRLTTNEVT 360
 Db 301 TCDLRIDGDCFMVSSEADTYRARMKCQRKGGVLAQIKSQKVQDILAFYLGRLTTNEVT 360

 Qy 361 DSDFETRNFWIGLTYKTAKDSFRWATGEHQAFSTFAFGQPDNHGLVWLSAAMGFGNCVEL 420
 Db 361 DSDFETRNFWIGLTYKTAKDSFRWATGEHQAFSTFAFGQPDNHGLVWLSAAMGFGNCVEL 420

 Qy 421 QASAAFNWNDQRCKTRNRYICQFAQEHISRWGPGS 455
 Db 421 QASAAFNWNDQRCKTRNRYICQFAQEHISRWGPGS 455

Sequence Alignment

Db . 1 MHPETSPGRGHLAVLLALGTAAAEVMPPOLOEOAPMAGALNRKESTLLSLHNRLRS 60C

Qy	61	WVQPPAAMRRLIMSDSLAOLARALGIPTPSLASGLMRTLOVMNOLLPAGLASF	120
Db	61	WVQPPAAMRRLIMSDSLAOLARALGIPTPSLASGLMRTLOVMNOLLPAGLASF	120
Qy	121	VEVYSIMFPAEGORTSHAAGECARNACTHYDOWATSSQJGCGRHLCSAQOTAIEAFVC	180
Db	121	VEVYSIMFPAEGORTSHAAGECARNACTHYDOWATSSQJGCGRHLCSAQOTAIEAFVC	180
Qy	181	AVSPGGNMEVNGKTIIPKKGAMCSLCTASVSGCFRMDHAGGLCEVYRANFCRMSCONHG	240
Db	181	AVSPGGNMEVNGKTIIPKKGAMCSLCTASVSGCFRMDHAGGLCEVYRANFCRMSCONHG	240
Qy	241	RLNISTCHCHCPRYTGVCYOVRCSLQCVHGREBEECSVCVDIGYGAOCATVYHPPH	300
Db	241	RLNISTCHCHCPRYTGVCYOVRCSLQCVHGREBEECSVCVDIGYGAOCATVYHPPH	300
Qy	301	TCDLRIDSCFVWSEADATYVYRANMCKQRKGVLQIKSKQVODILAFVYGRLETTREVT	360
Db	301	TCDLRIDSCFVWSEADATYVYRANMCKQRKGVLQIKSKQVODILAFVYGRLETTREVT	360
Qy	361	DSDFETRNFWICLTYKTKAKDSFRMATGEHOAFTSFAFGOPDNHGLVWLSPAMGQNCVEL	420
Db	361	DSDFETRNFWICLTYKTKAKDSFRMATGEHOAFTSFAFGOPDNHGLVWLSPAMGQNCVEL	420
Qy	421	QASAAFNWMDCKTRNNYTCQFAOEHISWGGSGS	455
Db	421	QASAAFNWMDCKTRNNYTCQFAOEHISWGGSGS	455
Qy	412	QASAAFNWMDCKTRNNYTCQFAOEHISWGGSGS	446
Db	412	QASAAFNWMDCKTRNNYTCQFAOEHISWGGSGS	446